Fig. 1.

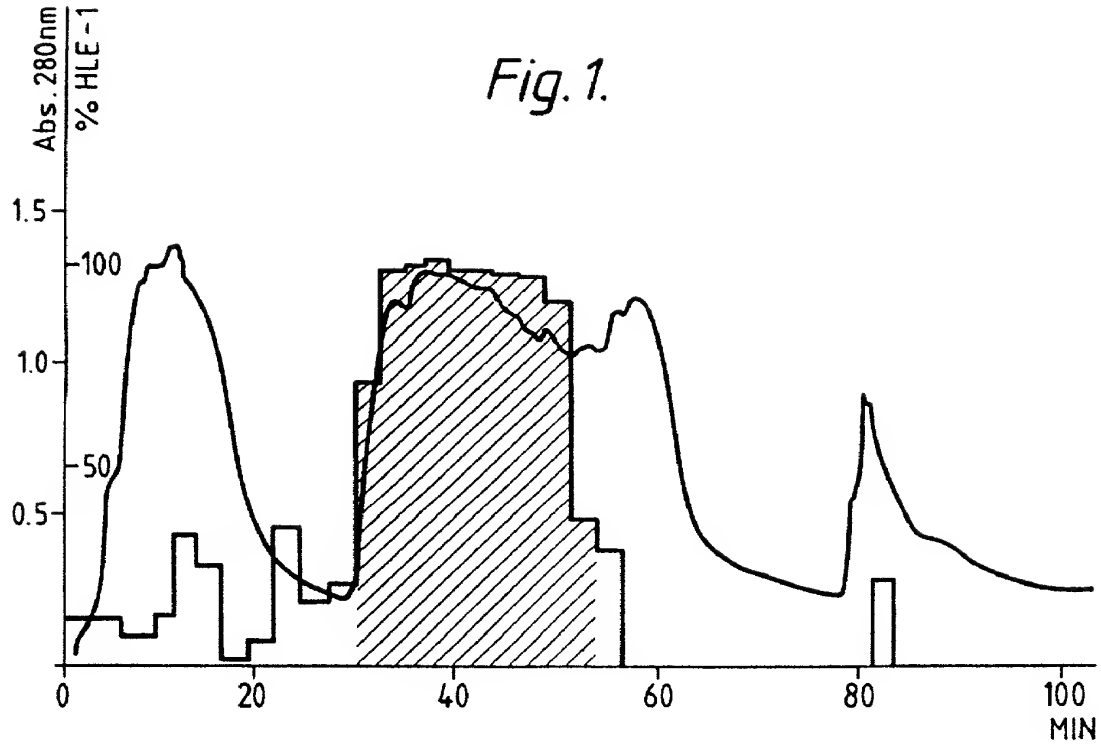

Abs. 280nm
% HLE-1
1.5
1.0
0.5
100
50
0
20
40
60
80
100
MIN

Fig. 2.

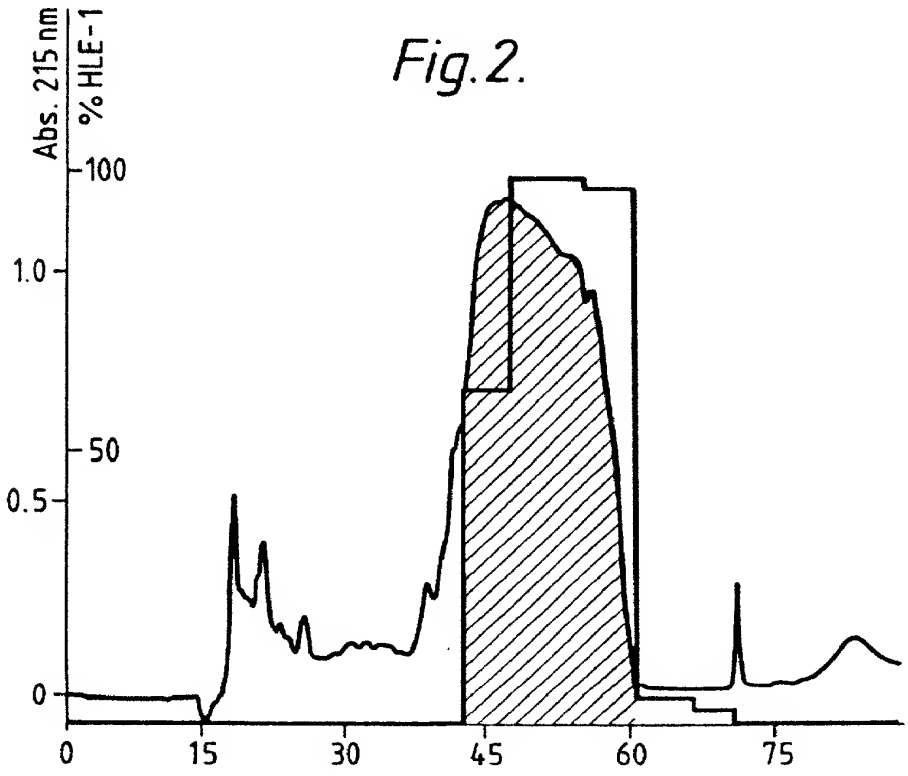

Abs. 215 nm
% HLE-1
100
1.0
50
0.5
0
0
15
30
45
60
75

Fig. 3.

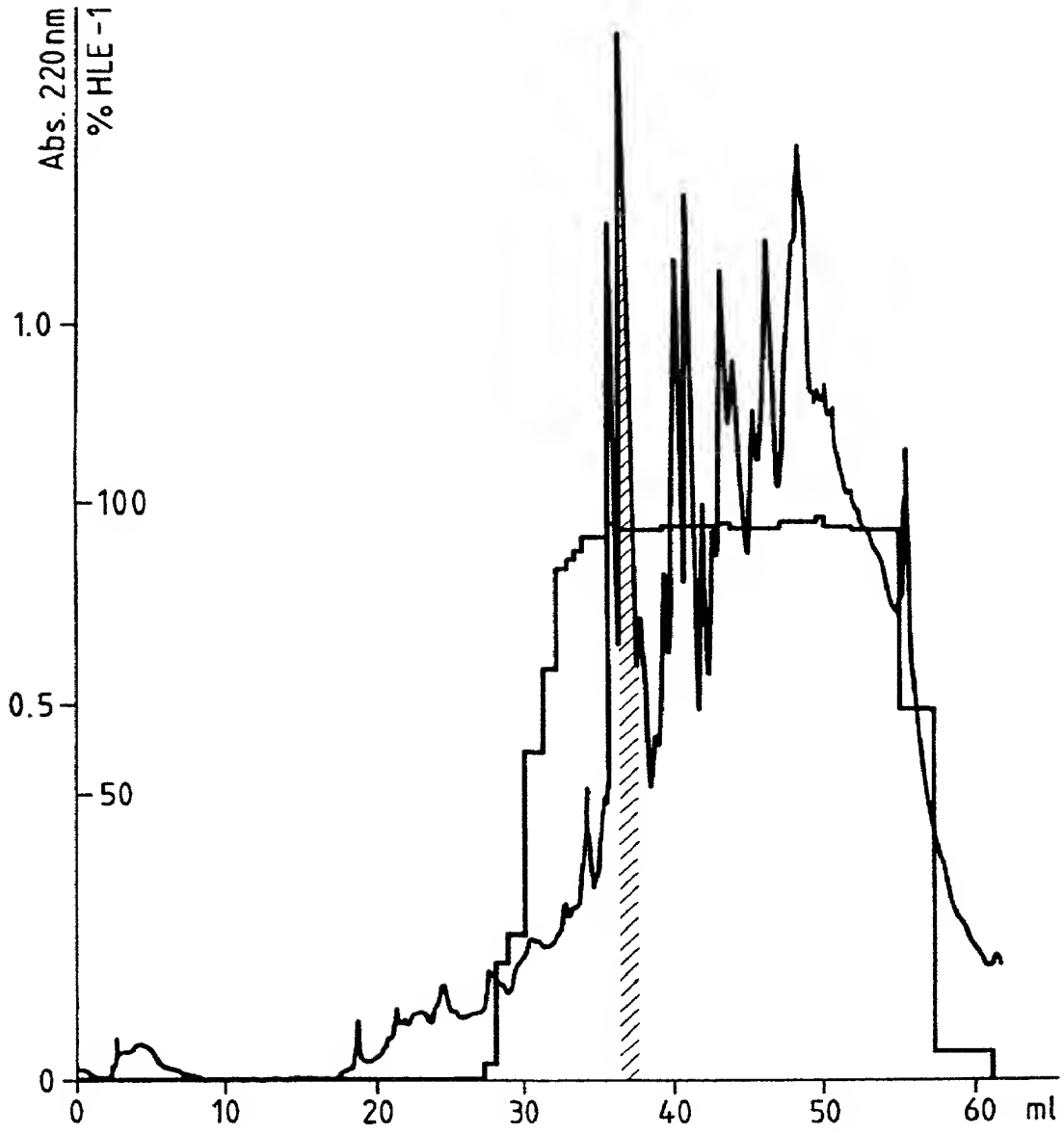


Fig. 4.

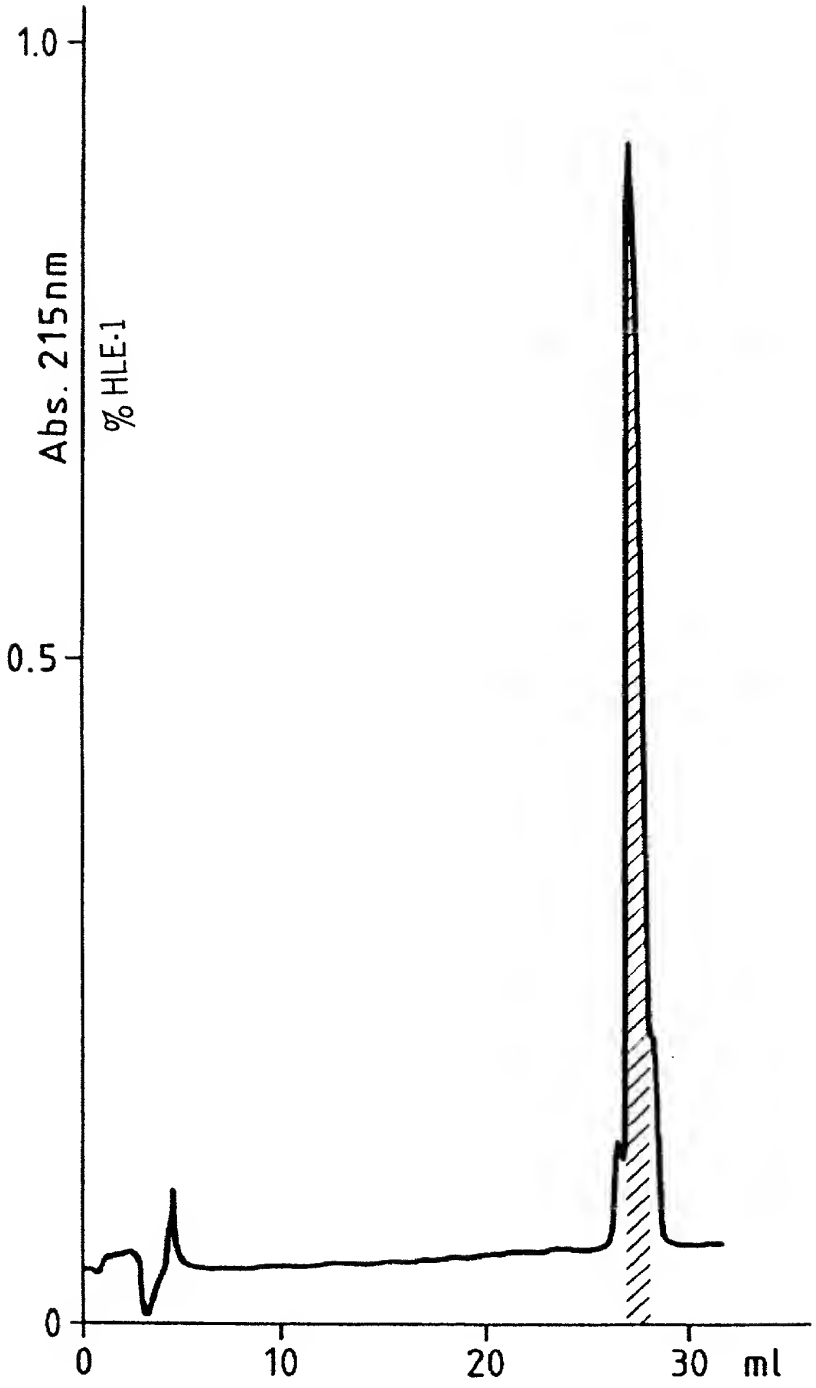


Fig. 5.

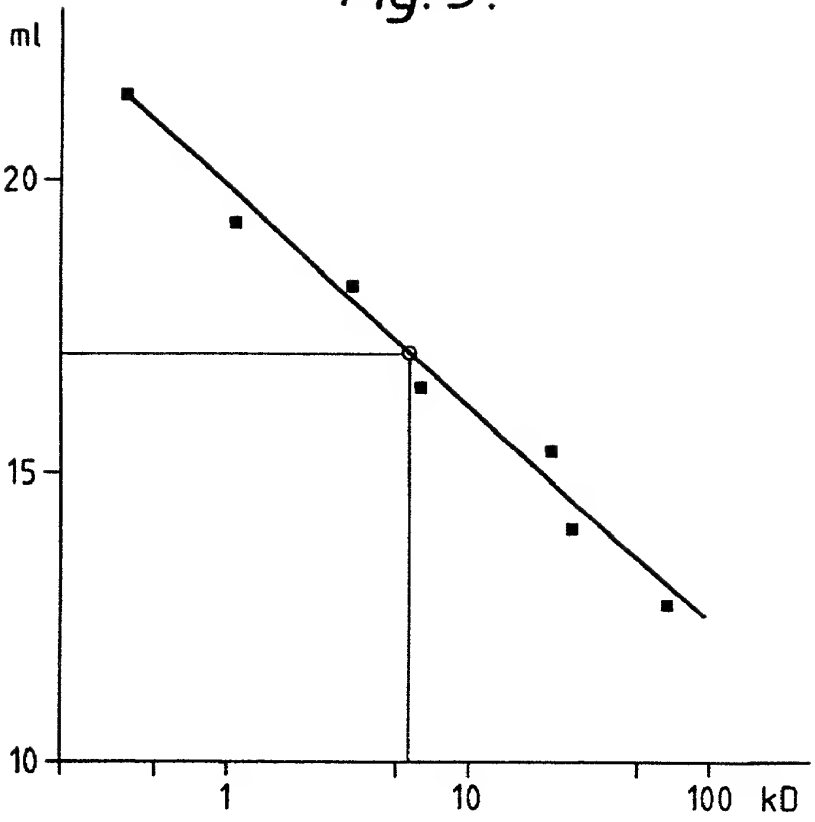


Fig. 7.

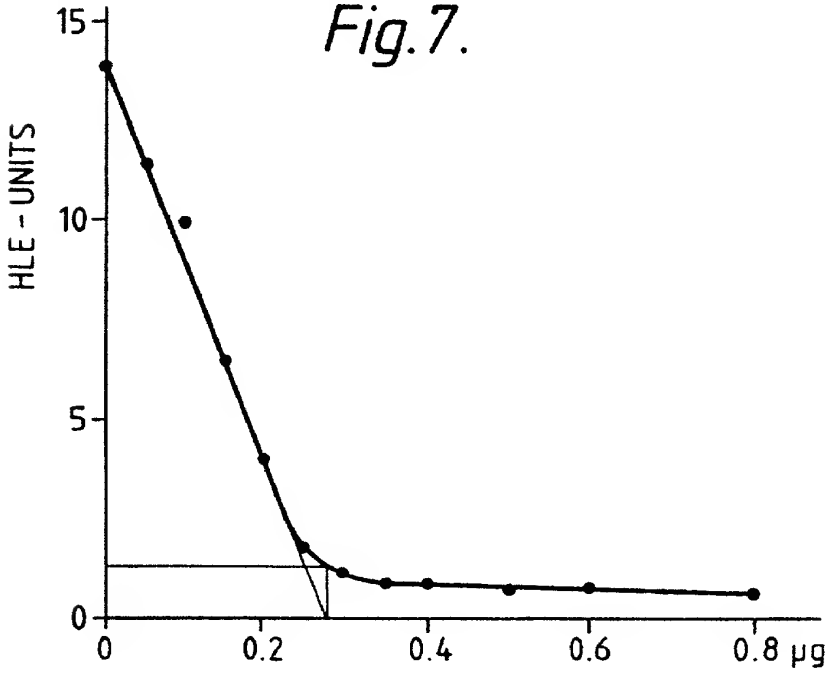


Fig.6.

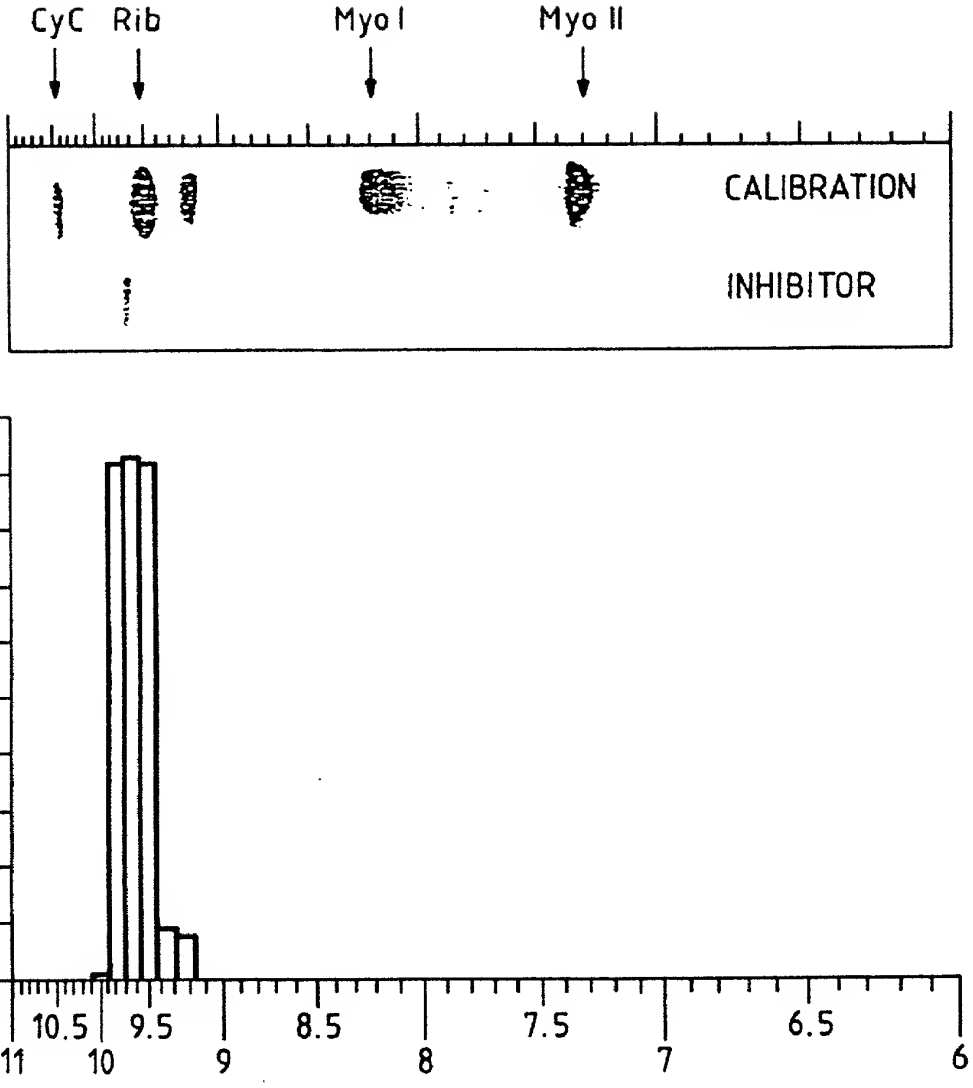

CyC
Rib
Myo I
Myo II
CALIBRATION
INHIBITOR
100
50
0
% HLE-1
10.5
9.5
8.5
7.5
6.5
pH 11
10
9
8
7
6

Fig.8.

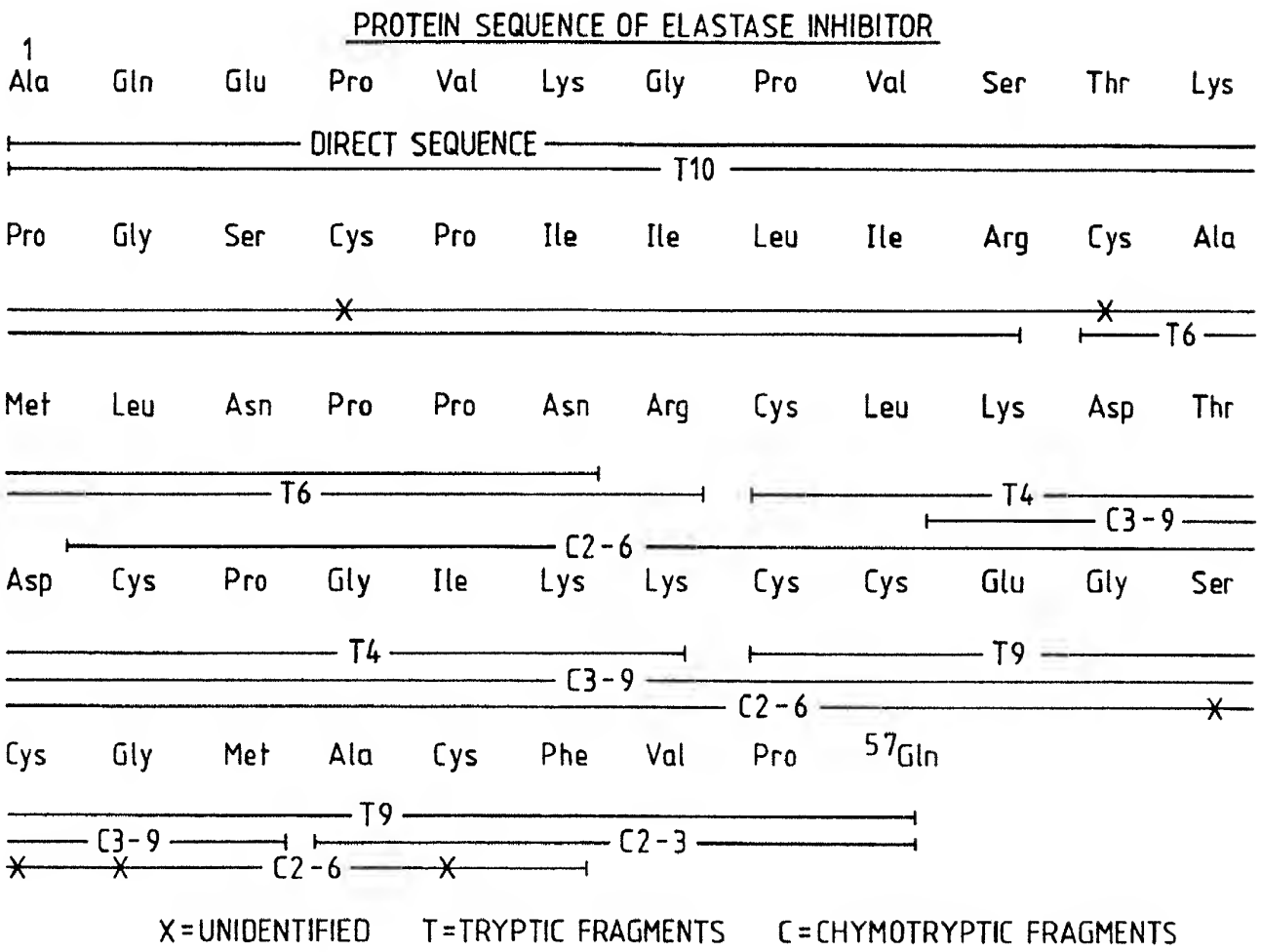


Fig. 9.

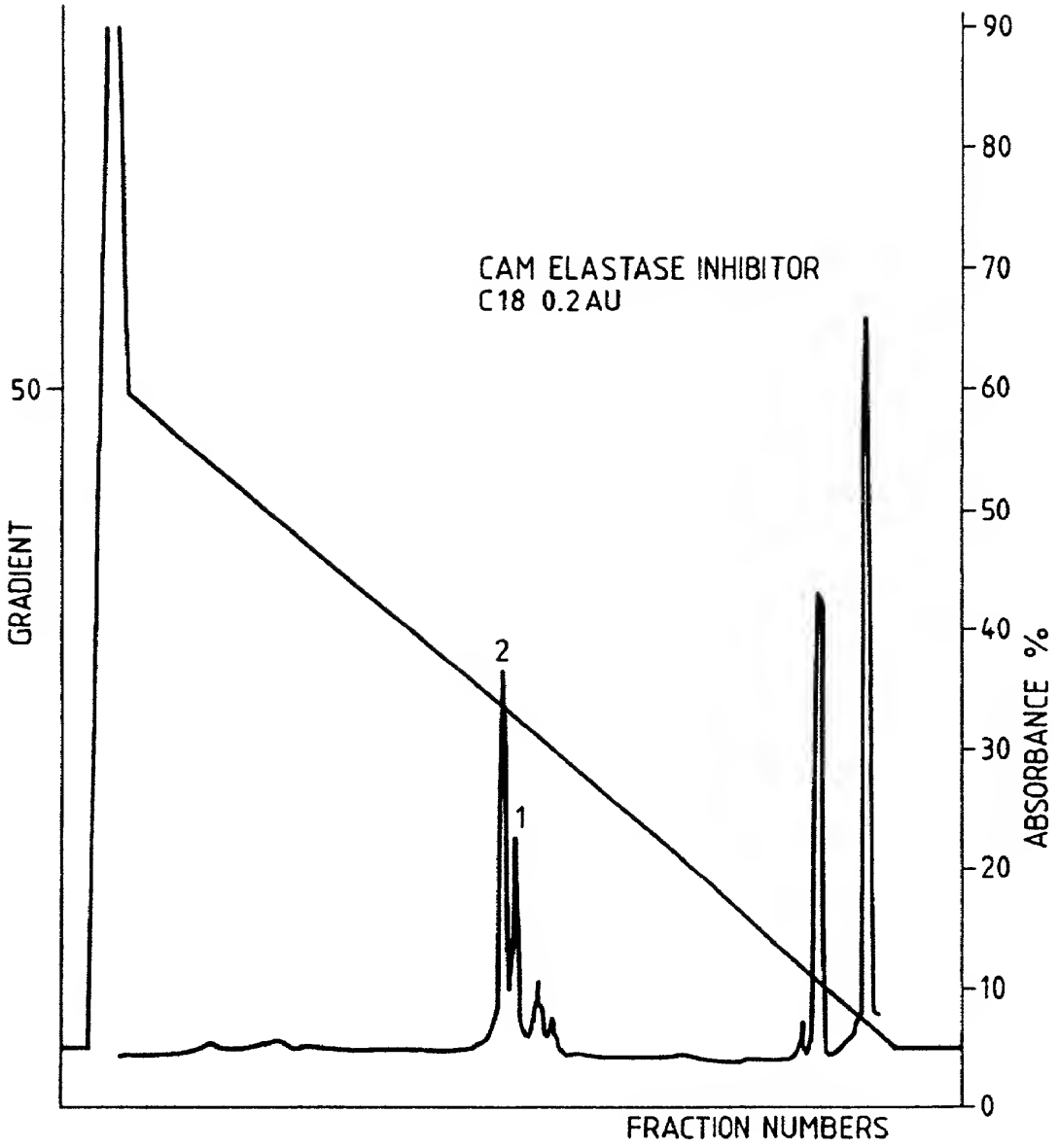

CAM ELASTASE INHIBITOR
C18 0.2AU
GRADIENT
50
ABSORBANCE %
90
80
70
60
50
40
30
20
10
0
2
1
FRACTION NUMBERS

Fig. 10.

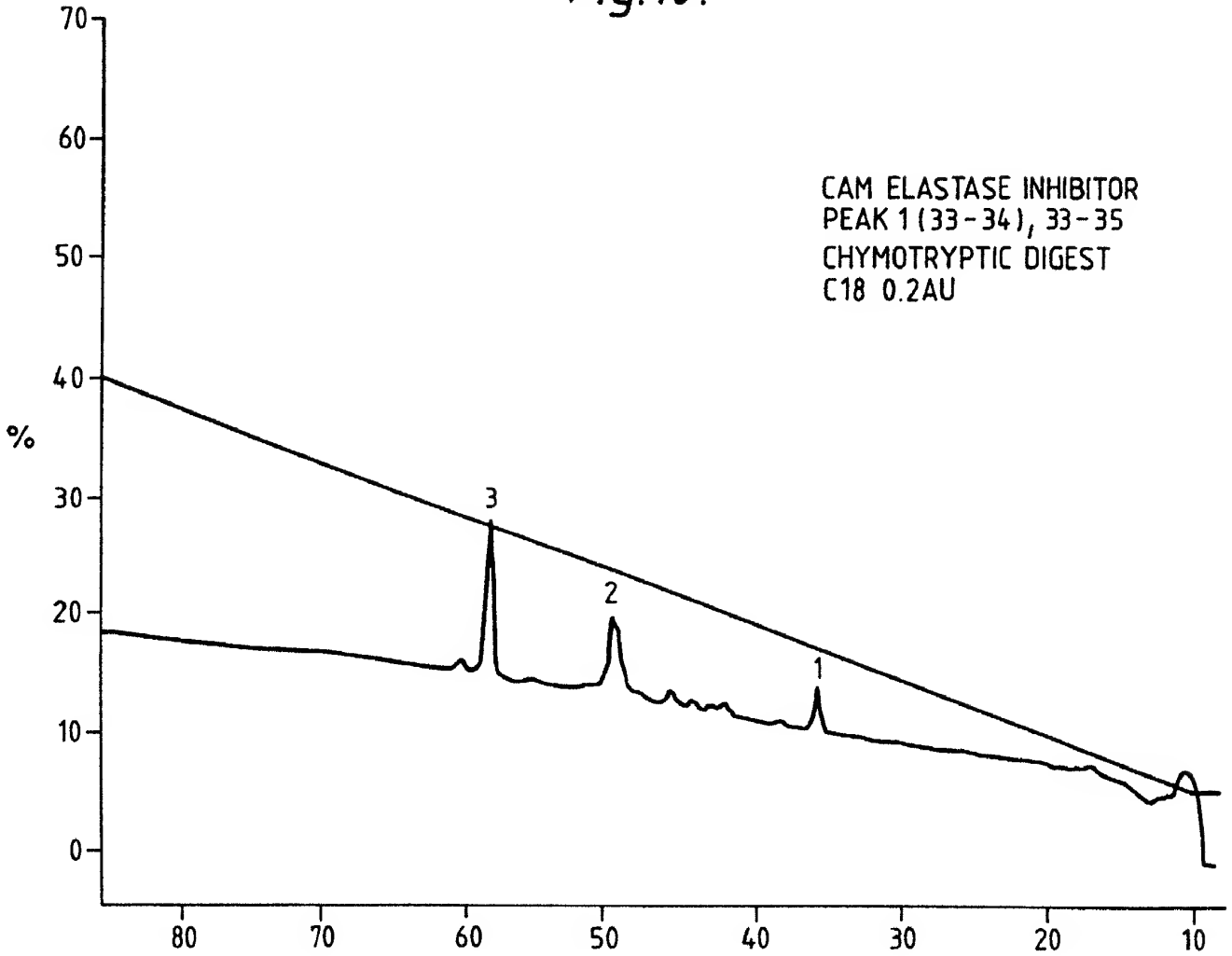


Fig. 11.

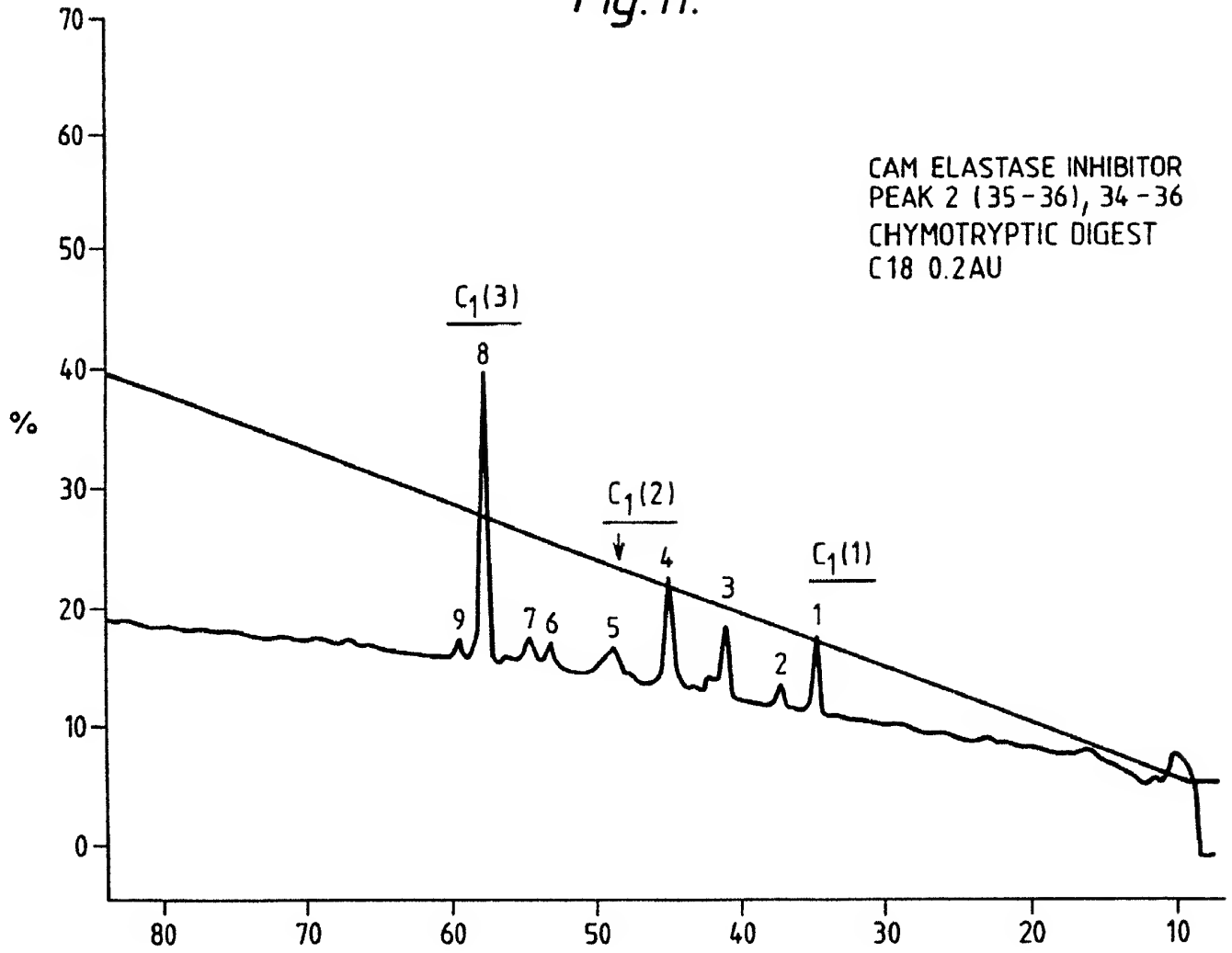


Fig. 12.

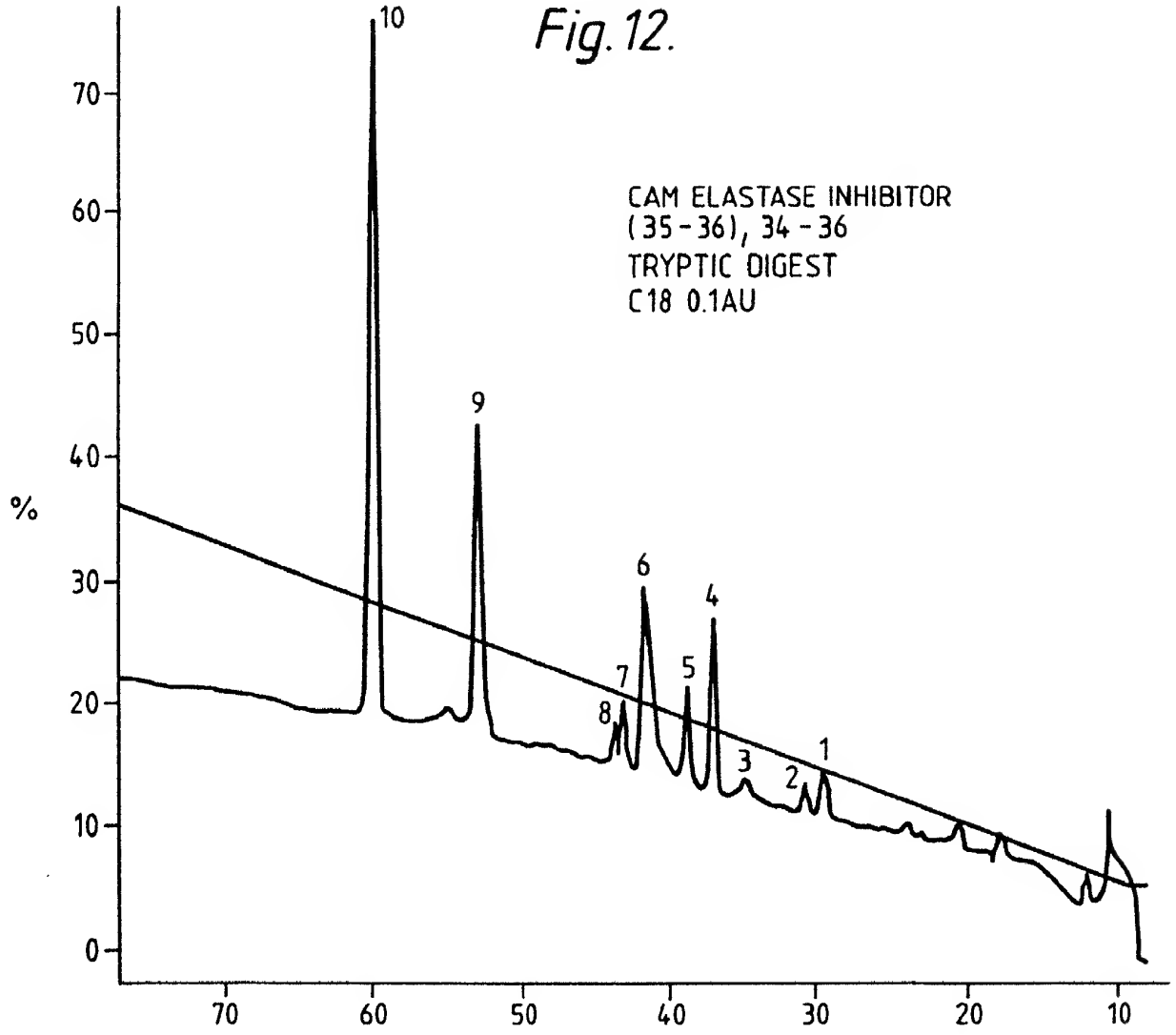


Fig. 13.

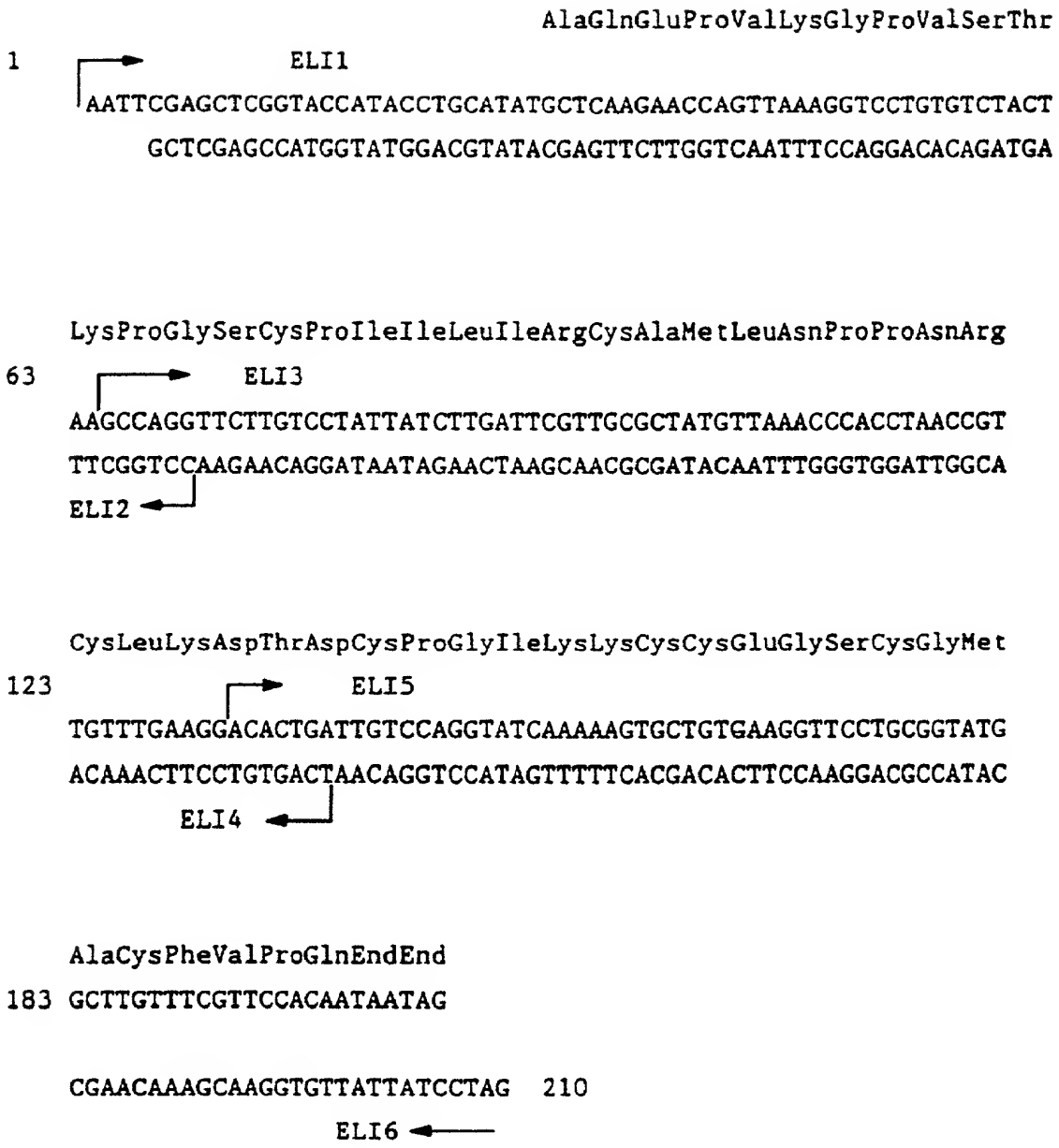

AlaGlnGluProValLysGlyProValSerThr
1
ELI1
AATTCGAGCTCGGTACCATACCTGCATATGCTCAAGAACCAGTTAAAGGTCCTGTGTCTACT
GCTCGAGCCATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGA
LysProGlySerCysProIleIleLeuIleArgCysAlaMetLeuAsnProProAsnArg
63
ELI3
AAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGT
TTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCA
ELI2
CysLeuLysAspThrAspCysProGlyIleLysLysCysCysGluGlySerCysGlyMet
123
ELI5
TGTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATG
ACAAACTTCCTGTGACTAACAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCATAC
ELI4
AlaCysPheValProGlnEndEnd
183 GCTTGTTTCGTTCCACAATAATAG
CGAACAAAGCAAGGTGTTATTATCCTAG 210
ELI6

Fig. 14.

Ala Gln Glu Pro Val Lys Gly Pro Val Ser Thr Lys Pro Gly Ser Cys

GCG CAA GAG CCA GTC AAA GGT CCA GTC TCC ACT AAG CCT GGC TCC TGC

5′ DNA

Sequence

Pro Ile Ile Leu Ile Arg Cys Ala Met Leu Asn Pro Pro Asn Arg Cys

CCC ATT ATC TTG ATC CGG TGC GCC ATG TTG AAT CCC CCT AAC CGC TGC

Leu Lys Asp Thr Asp Cys Pro Gly Ile Lys Lys Cys Cys Glu Gly Ser

TTG AAA GAT ACT GAC TGC CCA GGA ATZ AAG AAP TGC TGT GAA GGC TCT

Cys Gly Met Ala Cys Phe Val Pro Gln

TGC GGG ATG GCC TGT TTC GTT CCC CAG

Z = T, C or A

P = A or G

Fig. 19.

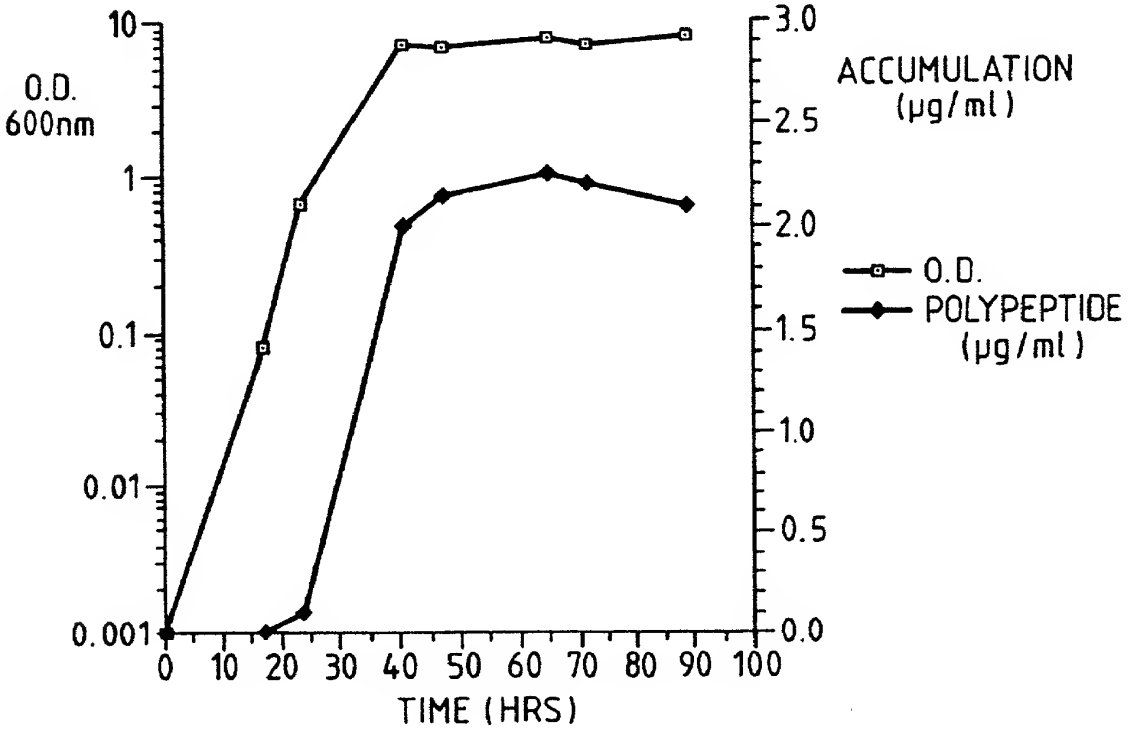


Fig. 15.

Ala Gln Glu Pro Val Lys Gly Pro Val Ser Thr Lys Pro Gly Ser Cys
GCG CAA GAG CCA GTC AAA GGT CCA GTC TCC ACT AAG CCT GGC TCC TGC
5' DNA
Sequence

Pro Ile Ile Leu Ile Arg Cys Ala Met Leu Asn Pro Pro Asn Arg Cys
CCC ATT ATC TTG ATC CGG TGC GCC ATG TTG AAT CCC CCT AAC CGC TGC

Leu Lys Asp Thr Asp Cys Pro Gly Ile Lys Lys Cys Cys Glu Gly Ser

TTG AAA GAT ACT GAC TGC CCA GGA ATZ AAG AAP TGC TGT GAA GGC TCT

Cys Gly Met Ala Cys Phe Val Pro Gln
TGC GGG ATG GCC TGT TTC GTT CCC CAG TAG GAGGGAGCCGGTCCTTGCTGCACCTGT

GCCGTCCCCAGAGCTACAGGCCCCATCTGGTCCTAAGTCCCTGCTGCCCTTCCCCTTCCCACACTGTCCA
TTCTTCCTCCCATTCAGGATGCCCACGGCTGGAGCTGCCTCTCTCATCCACTTTCCAATAAAGAGTTCCG
GAATTC

Poly A 3'
signal

Z = T, C or A
P = A or G

Fig. 16.

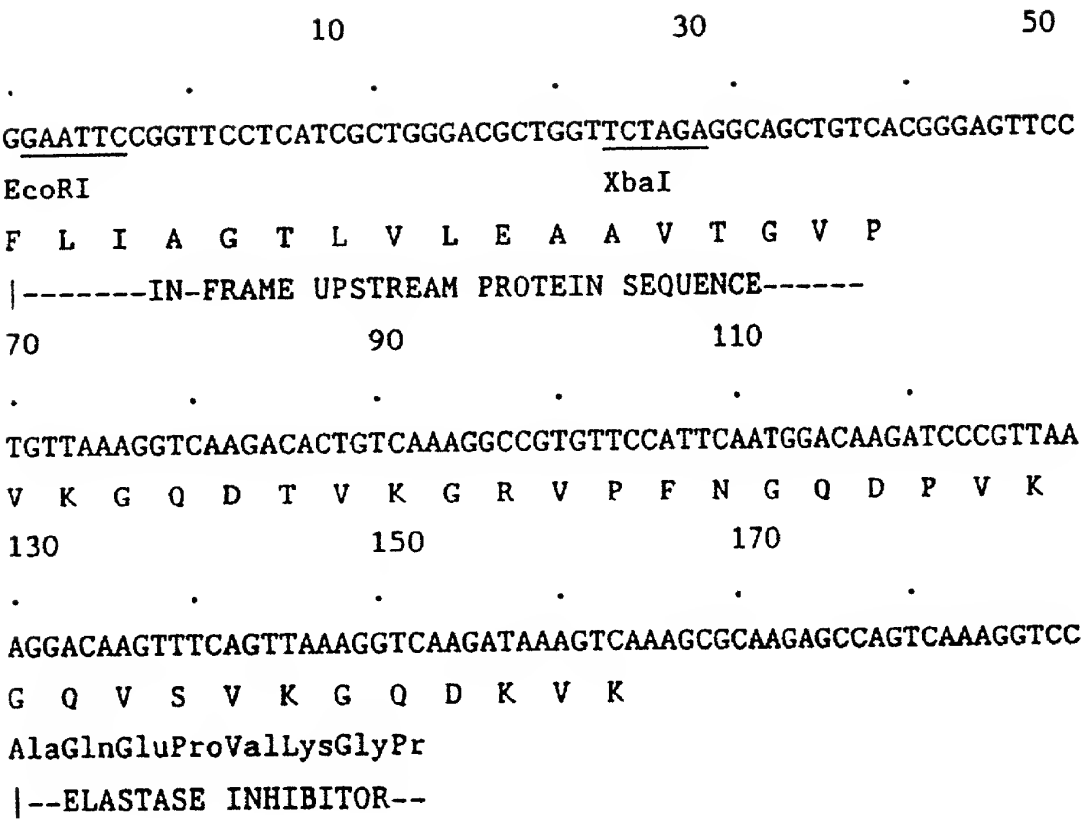
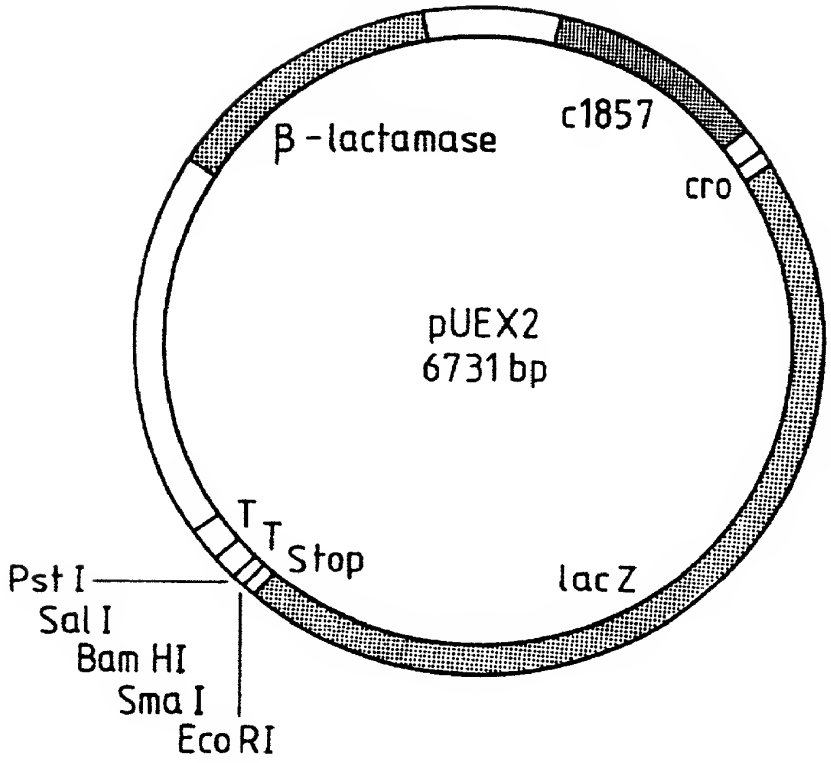

10
30
50
GGAATTCCGGTTCCTCATCGCTGGGACGCTGGTTCTAGAGGCAGCTGTCACGGGAGTTCC
EcoRI
XbaI
F L I A G T L V L E A A V T G V P
|-------IN-FRAME UPSTREAM PROTEIN SEQUENCE------
70
90
110
TGTTAAAGGTCAAGACACTGTCAAAGGCCGTGTTCCATTCAATGGACAAGATCCCGTTAA
V K G Q D T V K G R V P F N G Q D P V K
130
150
170
AGGACAAGTTTCAGTTAAAGGTCAAGATAAAGTCAAAGCGCAAGAGCCAGTCAAAGGTCC
G Q V S V K G Q D K V K
AlaGlnGluProValLysGlyPr
|--ELASTASE INHIBITOR--

Fig. 16 (cont.)

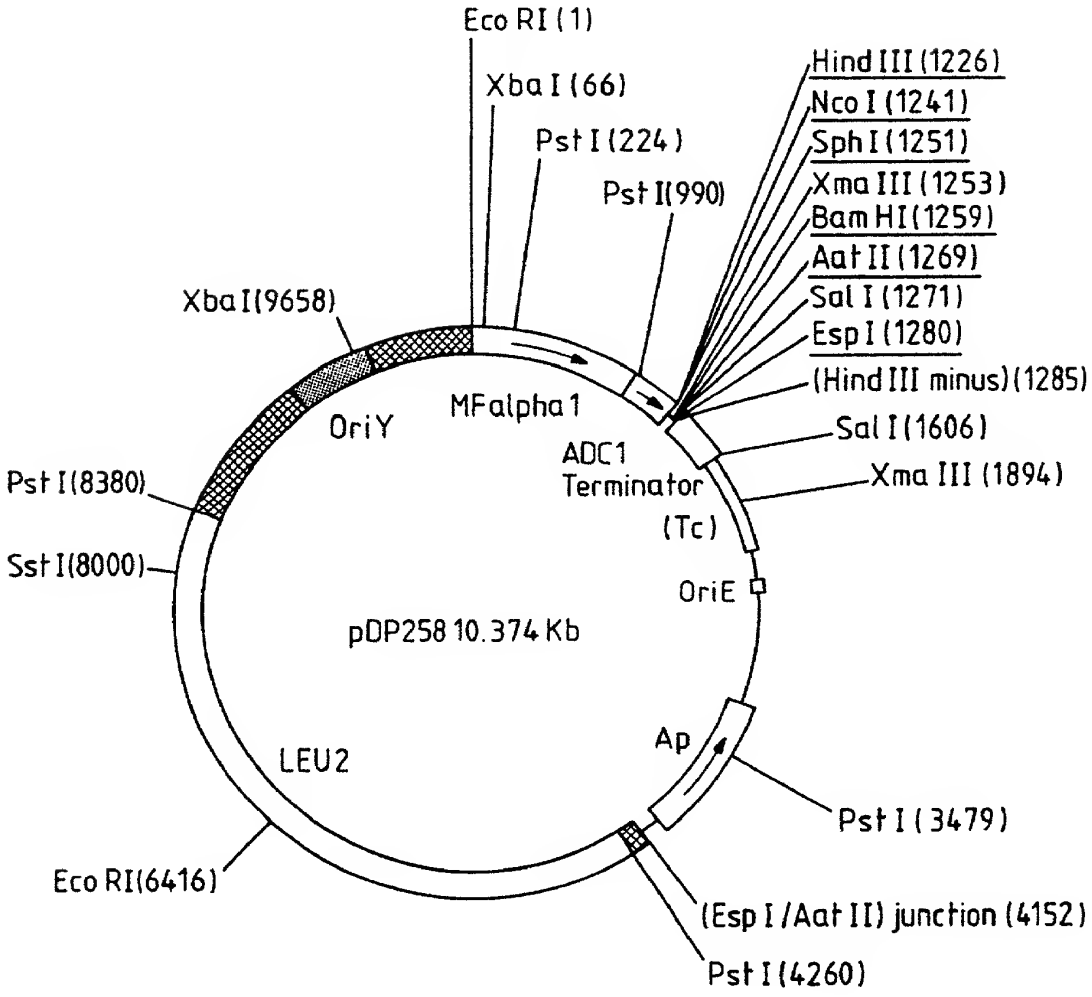
```
      190                 210                 230
       .         .         .         .         .         .
AGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTGATCCGGTGCGCCATGTTGAATCC
oValSerThrLysProGlySerCysProIleIleLeuIleArgCysAlaMetLeuAsnPr

      250                 270                 290
       .         .         .         .         .         .
CCCTAACCGCTGCTTGAAAGATACTGACTGCCCAGGAATCAAGAAGTGCTGTGAAGGCTC
oProAsnArgCysLeuLysAspThrAspCysProGlyIleLysLysCysCysGluGlySe
      310                 330                 350
       .         .         .         .         .         .
TTGCGGGATGGCCTGTTTCGTTCCCCAGTGAGAGGGAGCCGGTCCTTGCTGCACCTGTGC
rCysGlyMetAlaCysPheValProGlnEnd
      370                 390                 410
       .         .         .         .         .         .
CGTCCCCAGAGCTACAGGCCCCATCTGGTCCTAAGTCCCTGCTGCCCTTCCCCTTCCCAC

      430                 450                 470
       .         .         .         .         .         .
ACTGTCCATTCTTCCTCCCATTCAGGATGCCCACGGCTGGAGCTGCCTCTCTCATCCACT

      490
       .         .
TTCCAATAAAGAGTTCCGGAATTC
          Poly A          EcoRI
          signal
```

Fig. 17.




```
          EcoRI   SmaI BamHI    SalI          PstI
          |       |    |       |             |
pUEX2     GAA TTC CCG GGG ATC CGT CGA CCT GCA GCC AAG CTT GCT GAT TGA
          Glu Phe Pro Gly Ile Arg Arg Pro Ala Ala Lys Leu Ala Asp ***
```

Fig. 18.


Eco RI (1)
Xba I (66)
Pst I (224)
Pst I(990)
Hind III (1226)
Nco I (1241)
Sph I (1251)
Xma III (1253)
Bam HI (1259)
Aat II (1269)
Sal I (1271)
Esp I (1280)
(Hind III minus) (1285)
Sal I (1606)
Xma III (1894)
Xba I(9658)
OriY
MFalpha 1
ADC1
Terminator
(Tc)
Pst I(8380)
Sst I(8000)
OriE
pDP258 10.374 Kb
Ap
LEU2
Pst I (3479)
Eco RI(6416)
(Esp I /Aat II) junction (4152)
Pst I (4260)